

TITLE"PROTEIN ENGINEERING"FIELD OF THE INVENTION

This application is a 371  
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THIS INVENTION relates to a method of identifying proteins suitable for protein engineering. In particular, the present invention relates to a computer database searching method of identifying proteins according to aspects of three-dimensional structure, and furthermore to the modification of proteins so identified to thereby possess one or more desired characteristics. Although not limited thereto, this invention relates to engineered proteins such as cytokine mimetics.

BACKGROUND OF THE INVENTION

Proteins are central to life due to their crucial involvement in a variety of biological processes, such as enzyme catalysis of biochemical reactions, control of nucleic acid transcription and replication, hormonal regulation, signal transduction cascades and antigen recognition during immune responses.

In many cases, one or more structural regions of a protein are responsible for a particular function, hereinafter referred to as "*functional regions*". These regions may constitute the active site of a protein enzyme, the nucleic acid binding domain of a transcription factor, a region of a protein cytokine crucial to binding the specific receptor for that cytokine, or antigen-binding regions of antigen receptors.

A functional region of a protein usually comprises one or more amino acids which are required for that particular function, that is, they are essential for that function.

In many cases, although these required amino acid residues are topographically proximal to each other, they may be well separated with respect to primary amino acid sequence, that is, they are non-contiguous. In addition, where there is more than one functional region of a protein, these regions may also be topographically proximal, but well separated in terms of primary amino acid sequence. In some cases,

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